



UNITED STATES PATENT AND TRADEMARK OFFICE



UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/061,043	01/30/2002	David J. Glass	REG753B	8223

7590 04/16/2004

Laura J. Fischer
Regeneron Pharmaceuticals, Inc.
777 Old Saw Mill River Road
Tarrytown, NY 10591

EXAMINER

KERR, KATHLEEN M

ART UNIT PAPER NUMBER

1652

DATE MAILED: 04/16/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No. 10/061,043	Applicant(s) GLASS ET AL.	
	Examiner Kathleen M Kerr	Art Unit 1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 06 February 2004.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-3, 5-8 and 33-40 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1-3, 5-8 and 33-40 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☒ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. _____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- | | |
|--|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892) | 4) <input type="checkbox"/> Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 5) <input type="checkbox"/> Notice of Informal Patent Application (PTO-152) |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date <u>3/17/03</u> . | 6) <input checked="" type="checkbox"/> Other: <u>alignments</u> (3) |

DETAILED ACTION

Application Status

1. In response to the previous Office action, a written restriction requirement (mailed on January 21, 2004), Applicants filed a response and amendment received on February 6, 2004. Said amendment cancelled Claims 4 and 9-32, amended Claims 1-3, 5, and 6, and added new Claims 33-40. Thus, Claims 1-3, 5-8, and 33-40 are pending in the instant Office action.

Election

2. Applicant's election of Group III, Claims 1-3 and 5-8 related to SEQ ID NO:34 in a paper received on February 6, 2004 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (M.P.E.P. § 818.03(a)). Applicants have amended Claims 1-3 and 5-8 to be limited to the elected subject matter. Moreover, new Claims 33-40 would fall within the elected Group and will be examined herein. Thus, Claims 1-3, 5-8, and 33-40 are pending in the instant application and will be examined herein.

Information Disclosure Statement

3. The information disclosure statement filed on March 17, 2003 has been reviewed, and its references have been considered as shown by the Examiner's initials next to each citation on the attached copy.

Compliance with the Sequence Rules

4. By virtue of the sequence listing filed on January 27, 2003, in computer readable form and paper copy containing 48 sequences, the instant application now fully complies with the sequence rules.

Objections to the Specification

5. The specification is objected to because the title is not descriptive. A new title is required that is clearly indicative of the invention to which the elected claims are drawn (see M.P.E.P. § 606.01). The Examiner suggests the following new title:

---Nucleic Acid Molecules encoding MAFBX, a protein related to Ubiquitin Ligase---

6. In the specification, the Abstract is objected to for not completely describing the disclosed subject matter (see M.P.E.P. § 608.01(b)). It is noted that in many databases and in foreign countries, the Abstract is crucial in defining the disclosed subject matter, thus, its completeness is essential. The Examiner suggests the inclusion of the specific source species, human and rat, for completeness. Also, the term “MAFBXpathw” at the end of the Abstract is unclear and may be a typographical error. Correction and/or clarification are required.

7. The specification is objected to for being confusing concerning the nature of MA-61 and MAFBX. The terms seem to be used interchangeable. If they are, in fact, the same protein, a statement to that effect is required in the Abstract and in their first occurrence in the specification.

Art Unit: 1652

8. The specification is objected to for having improper citations as follows:
- On page 3, line 27, "Winston, 1999" must identify *---supra---* to indicate that the full citation can be found earlier in the specification.
 - On page 4, line 9, the citation of "Newey, in press" is incomplete and, thus, an improper incorporation by reference (see first paragraph of the specification); deletion is required.
 - On page 49, line 14, the citation of Kipreos is incomplete; completion is required and amendable since the complete reference is indicated clearly by the incomplete citation.

Correction is required for all of the above points.

9. The specification is objected to for the following unclear use of sequence numbers:
- On page 12, the description of Figure 4. These numbers seem indicative of residues of a protein, but the specific protein referred to is unclear and should be referred to by name as well as SEQ ID NO.
 - On page 45, line 31. Reference to residue numbers is found without any reference to the specific sequence (SEQ ID NO) to which they are related.
 - On pages 47-48, bridging paragraph. Reference to nucleotide numbers is found without any reference to the specific sequence (SEQ ID NO) to which they are related.
 - On pages 54, line 3. Reference to nucleotide numbers is found without any reference to the specific sequence (SEQ ID NO) to which they are related.

Correction is required for all of the above points.

10. The specification is objected to for having unclear descriptions of and/or references to Figures as follows:

- On page 13, the description of Figure 13 is confusing because the figure actually names the sequence SEQ ID NO:10 while the description notes the sequences as SEQ ID NO:27.
- On pages 14-15, the description of Figures 27-31 is unclear. The first sentence describes Figure 27A and the second describes Figure 27B; both sentences do not describe both 27A and 27B as written. This confusion is reiterated for Figures 28-31.
- On page 42, line 4, reference to Figure 1A is confusing since no Figure 1A is in the specification.
- On page 43, references to Figures 2B, 2C, and 2D are confusing since only one panel in Figure 2 is found.

Art Unit: 1652

- e) On page 45, references to Figures 3A and 3B are confusing since only one panel in Figure 3 is found.
 - f) On page 47, references to Figure 4C are confusing since only one panel in Figure 4 is found. On page 49, references to Figure 4B are confusing since only one panel in Figure 4 is found.
 - g) On pages 50 and 51, references to Figures 5B-C and 6A-C are unclear.
 - h) On the noted pages, references to Figures 27-31 as, for example, "Figures 27A-27BA" and "Figures 27A-27BB" are confusing since these Figures are A-B and not BA or BB. Pages 42, 43, 45, 46, and 52-54.
 - i) On page 45, line 8, the notation of "right" is unclear if not specifically referring to a figure.
 - j) On page 49, line 34, reference to Figure 5A is incorrect; the correct reference is to Figure 27A. This same correction is necessary on page 50, line 35.
- Correction on all of the above points is required.

11. The specification is objected to for not having updated US patent information. On page 55, reference to a US application, 09/732,234, must be updated to the USPN 6,586,251.

Correction is required.

12. The specification is objected to for improper citation of a trademark. On page 7, line 32, the use of the trademark "Taqman" has been noted. It should be capitalized wherever it appears and be accompanied by the generic terminology.

Although the use of trademarks is permissible in patent applications, the proprietary nature of the marks should be respected and every effort made to prevent their use in any manner, which might adversely affect their validity as trademarks.

Claim Objections

13. Claims 2 are objected to for improper format of a Markush group. In Claim 1, items a and b must be linked by the conjunction ---and--- (as filed, no conjunction is in the claim) to

Art Unit: 1652

identify the group selected from. In Claim 2, items b and c must be linked by the conjunction --- and--- (as filed, “or” is in the claim between items b and c) to identify the group selected from.

Correction is required.

14. Claim 3 is objected to under 37 C.F.R. § 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form. The parent claim, Claim 1, requires an exact sequence, within the degeneracy of the genetic code while Claim 3 limits to any molecule that hybridizes under particular conditions without any limitation of encoding.

Claim Rejections - 35 U.S.C. § 112

The following is a quotation of the second paragraph of 35 U.S.C. § 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

15. Claims 2 and 5-8 are rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The structure of the preamble is confusing. The requirement to encode “MAFBX” is unclear since only one sequence, SEQ ID NO:35, is disclosed as MAFBX; however, the scope of the variation of items b and c indicate that SEQ ID NO:35 need not be exactly encoded to meet all the limitations of the claim. In the preamble, it is also unclear if the fragment is limited by the requirements of a-c or if a fragment of something meeting the limitations of a-c is all that is required.

Art Unit: 1652

The term “stringent conditions” is unclear. On page 6, the specification describes what stringent conditions “may include” but a definite statement of what these conditions are is lacking in the specification and/or the claims.

The “biological activity of MAFBX” is unclear. On page 1, MA-61 (another apparent name for MAFBX) is described as “novel substrate-targeting subunits of ubiquitin ligases”; however, a definite function is not ascribed to MAFBX. Acting as a subunit is not considered a function of a molecule. If some binding function and/or some catalytic function is required to be an MAFBX, such function(s) should be made clear.

Item (c) is wholly confusing. Is the phrase “but for the degeneracy of the genetic code” intended to mean that that nucleotide sequence of item c does not hybridize but if it were altered within the degeneracy of the genetic code it now would hybridize? Also, the term “hybridize” used in item c has no definition; the Examiner notes that all nucleotide sequences hybridize to some extent to each other based on their inherent polar nature.

Clarification on all these points is required.

16. Claims 3 and 33-36 are rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The phrase “derived from” is unclear. Must the nucleic acid molecules claimed be native to a mammalian genome? The term “derived from” can indicate recombinant biology techniques to alter a sequence wherein this phrase does not limit to molecules that are mammalian in origin.

Art Unit: 1652

The term “stringent conditions” is unclear. On page 6, the specification describes what stringent conditions “may include” but a definite statement of what these conditions are is lacking in the specification and/or the claims.

The inclusion of a ring domain is confusing in a molecule related to MAFBX since MAFBX is disclosed as having an F-box domain, not a ring domain as found in MURF1 and MURF3 (see page 4). Moreover, the structure of a ring domain is unclear since the specification provides only functional description (see page 3).

Clarification on all these points is required.

The following is a quotation of the first paragraph of 35 U.S.C. § 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

17. Claims 2, 3, 5-8, and 33-36 are rejected under 35 U.S.C. § 112, first paragraph, written description, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The instant claims are drawn to nucleic acid molecules encoding MAFBX polypeptides with unclear functional limitations and limited and/or unclear structural limitations.

The Court of Appeals for the Federal Circuit has recently held that a “written description of an invention involving a chemical genus, like a description of a chemical species, ‘requires a precise definition, such as be structure, formula [or] chemical name,’ of the claimed subject matter sufficient to distinguish it from other materials.” *University of California v. Eli Lilly and*

Art Unit: 1652

Co., 1997 U.S. App. LEXIS 18221, at *23, quoting *Fiers v. Revel*, 25 USPQ2d 1601, 1606 (Fed. Cir. 1993) (bracketed material in original). To fully describe a genus of genetic material, which is a chemical compound, applicants must (1) fully describe at least one species of the claimed genus sufficient to represent said genus whereby a skilled artisan, in view of the prior art, could predict the structure of other species encompassed by the claimed genus and (2) identify the common characteristics of the claimed molecules, e.g., structure, physical and/or chemical characteristics, functional characteristics when coupled with a known or disclosed correlation between function and structure, or a combination of these.

In the instant specification, a nucleic acid molecule encoding MAFBX is described in the form of SEQ ID NO:34, which encodes SEQ ID NO:35, a 355 amino acid protein. The specification fully describes the genus relating to said SEQ ID NOs with sequence identity limitations. However, the absence of clear structural limitations and clear functional limitations renders the instant claims broad enough to encompass virtually any DNA sequence with a mild affinity for SEQ ID NO:34. The genus of the instant claims contains polynucleotides within the sequence identity limitations, but having different function, and the specification does not describe such polynucleotides. Applicants have not fully described a genus that has sequence identity limitations in the absence of functional limitations.

The Examiner suggests clear structural and functional limitations on the claimed nucleic acid molecules to overcome the instant rejection.

18. Claims 2, 3, 5-8, and 33-36 are rejected under 35 U.S.C. § 112, first paragraph, scope of enablement, because the specification, while being possibly enabling nucleic acid molecules that encode SEQ ID NO:35, does not reasonably provide enablement for nucleic acid molecules with

Art Unit: 1652

some structural (although unclear) and functional (also unclear) relationship to SEQ ID NO:34/35. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make the invention commensurate in scope with these claims. To make the claimed nucleic acid molecules to the full extent of the claimed scope would require undue experimentation.

The factors to be considered in determining whether undue experimentation is required are summarized in *re Wands* 858 F.2d 731, 8 USPQ2d 1400 (Fed. Cir, 1988). The Court in *Wands* states: "Enablement is not precluded by the necessity for some experimentation such as routine screening. However, experimentation needed to practice the invention must not be undue experimentation. The key word is 'undue,' not 'experimentation.'" (Wands, 8 USPQ2d 1404). Clearly, enablement of a claimed invention cannot be predicated on the basis of quantity of experimentation required to make or use the invention. "Whether undue experimentation is needed is not a single, simple factual determination, but rather is a conclusion reached by weighing many factual considerations." (Wands, 8 USPQ2d 1404). The factors to be considered in determining whether undue experimentation is required include: (1) the quantity of experimentation necessary, (2) the amount or direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claims. While all of these factors are considered, a sufficient amount for a *prima facie* case is discussed below.

Applicants present no guidance or working examples of the use of polynucleotides that have such low sequence identity with respect to SEQ ID NO:34. The nature of the invention is

Art Unit: 1652

such that the DNA encodes a functional protein, an MAFBX involved in ubiquitination; and with such a great deviation from the known sequence, the predictability of functionality becomes extremely low. Such enormous breadth and unpredictability renders the instant claims not enabled to the full extent of their scope without undue experimentation. Additionally, the instant specification teaches SEQ ID NO:35, an MAFBX ubiquitin ligase subunit protein from human, and SEQ ID NO:34, a human gene exactly encoding SEQ ID NO:35. The art includes no examples of MAFBX encoding genes. The art fully enables any DNA encoding SEQ ID NO:35 based on the degeneracy of the genetic code. While the instant specification describes and enables means for identifying other MAFBX genes using hybridization methods, etc., these methods do not enable one of skill in the art to make all, or a relevant portion of, the polynucleotides within the scope of the claims because the ability to find a MAFBX gene, which is structurally related to SEQ ID NO:34, is not equivalent to the ability to make an MAFBX gene as required by the statute (i.e., "make and use"). No description in the specification or the art provides particular residues whose encoding is important within the disclosed sequence so that its MAFBX-nature is maintained. Thus, one of skill in the art would be unable to predict the structure of the other members of the genus in order to make such members. Therefore, the instant claims are not enabled to the full extent of their scope.

19. Claims 7-8 are rejected under 35 U.S.C. § 112, first paragraph, scope of enablement, because the specification, while being possibly enabling host-vector systems for the production of MAFBX wherein an expression vector is used, does not reasonably provide enablement for systems wherein a vector other than an expression vector is used. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly

Art Unit: 1652

connected, to make the invention commensurate in scope with these claims. To make host vector systems for expression in the absence of expression vectors would require undue experimentation as summarized in the Wands factors above.

The nature of the host-vector system claimed is the MAFBX protein production is required. Expression vectors, such as found in Claims 6, 34, and 38, are appropriate for such systems. The specification has not taught, by way of examples or guidance, how to produce host-vector systems that produce MAFPX in the absence of expression vectors. Thus, the specification has not taught how to make the full scope of the claimed invention.

Claim Rejections - 35 U.S.C. § 101

35 U.S.C. § 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

20. Claims 1-3, 5-8, and 33-40 are rejected under 35 U.S.C. § 101 because the claimed invention lacks patentable utility. To fulfill the utility requirement of 35 U.S.C. § 101, an invention must have a specific, substantial, and credible utility, which is disclosed in the specification, or which is well established as considered by one of ordinary skill in the art. While MAFBX is described as being linked to muscle atrophy and other wasting diseases, no specific and/or substantial utility has been set forth in the specification (or the art) that constitutes a real-world use for the claimed nucleic acid molecules. Thus, the instant claims lack a patentable utility.

Claims 1-3, 5-8, and 33-40 are also rejected under 35 U.S.C. § 112, first paragraph, enablement. Specifically, since the claimed invention is not supported by either a specific and/or

Art Unit: 1652

substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Claim Rejections - 35 U.S.C. § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. § 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

21. Claims 1-3, 5-8, and 33-40 are rejected under 35 U.S.C. § 102(a) as being anticipated by Yue *et al.* (WO 00/70047). The instant claims are drawn to polynucleotides encoding SEQ ID NO:35 and related products.

Yue *et al.* teach sequence 106 which exactly encodes SEQ ID NO:35 and a portion of which is identical to SEQ ID NO:34 (see attached alignments). Yue *et al.* also teach expression vectors and host cells (see Abstract).

22. Claims 2, 3, 5-8, and 33-36 are rejected under 35 U.S.C. § 102(e) as being anticipated by Goldberg *et al.* (USPAP 2003/0077288). The instant claims are drawn to polynucleotides similar to nucleic acid sequences encoding SEQ ID NO:35 and related products.

Goldberg *et al.* teach a nucleic acid molecule encoding mouse atrophin-1, an F-box protein related to muscle wasting (see Abstract and page 4). Said nucleic acid molecule encodes

Art Unit: 1652

a protein that is about 97% identical to SEQ ID NO:35 and is 90% identical to SEQ ID NO:34 (see attached alignment). Goldberg *et al.* teach expression systems in host cells (see page 2).

23. Claims 2, 3, 5-8, and 33-36 are rejected under 35 U.S.C. § 102(e) as being anticipated by Rosen *et al.* (USPAP 2002/0151681). The instant claims are drawn to polynucleotides similar to nucleic acid sequences encoding SEQ ID NO:35 and related products.

Rosen *et al.* teach SEQ ID NO:66, which is 82% identical to SEQ ID NO:34, and which encodes a protein that is 80% identical to SEQ ID NO:35. SEQ ID NO:66 almost exactly encodes residues 62-355 of SEQ ID NO:35 (missing the N-terminus) (see attached alignment). The Examiner notes that SEQ ID NO:66 has priority to at least March 8, 2000 by way of PCT/US00/05988 (WO 200055174). Rosen *et al.* also teach expression systems in host cells (see Abstract).

24. Claims 2, 3, 5-8, and 33-36 are rejected under 35 U.S.C. § 102(e) as being anticipated by Tang *et al.* (USPN 6,569,662). The instant claims are drawn to polynucleotides similar to nucleic acid sequences encoding SEQ ID NO:35 and related products.

Tang *et al.* teach SEQ ID NO:1011, which is 61% identical to SEQ ID NO:34, and which encodes a protein that is 60% identical to SEQ ID NO:35. SEQ ID NO:1011 almost exactly encodes residues 1-217 of SEQ ID NO:35 (missing the C-terminus) (see attached alignment). Tang *et al.* also teach expression systems in host cells (see column 3).

Art Unit: 1652

Conclusion

25. Claims 1-3, 5-8, and 33-40 are not allowed for the reasons identified in the numbered sections of this Office action. Applicants must respond to the objections/rejections in each of the numbered sections in this Office action to be fully responsive in prosecution.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Kathleen M Kerr whose telephone number is (571) 272-0931.

The examiner can normally be reached on Monday through Friday, from 9:00am to 6pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathupura Achutamurthy can be reached on (571) 272-0928. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).



Kathleen M Kerr
Examiner
Art Unit 1652

April 14, 2004

ALIGNMENT

LOCUS AR339520 828 bp DNA linear PAT 17-AUG-2003
 DEFINITION Sequence 1011 from patent US 6569662.
 ACCESSION AR339520
 VERSION AR339520.1 GI:33726377
 REFERENCE 1 (bases 1 to 828)
 AUTHORS Tang, Y.T., Zhou, P. and Drmanac, R.T.
 TITLE Nucleic acids and polypeptides
 JOURNAL Patent: US 6569662-A 1011 27-MAY-2003;

Query Match 61.0%; Score 649.4; DB 6; Length 828;
 Best Local Similarity 99.8%; Pred. No. 2.7e-152;
 Matches 650; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGCCATTCCTCGGGCAGGACTGGCGGTCCCCGGGCAGAACTGGGTGAAGACGGCCGAC	60
Db	45	ATGCCATTCCTCGGGCAGGACTGGCGGTCCCCGGGCAGAACTGGGTGAAGACGGCCGAC	104
Qy	61	GGCTGGAAGCGCTTCTTGATGAGAAGAGCGGCAGTTTCGTGAGCGACCTCAGCAGTTAC	120
Db	105	GGCTGGAAGCGCTTCTTGATGAGAAGAGCGGCAGTTTCGTGAGCGACCTCAGCAGTTAC	164
Qy	121	TGCAACAAGGAGGTATACAATAAGGAGAATCTTTTCAACAGCCTGAACTATGATGTTGCA	180
Db	165	TGCAACAAGGAGGTATACAATAAGGAGAATCTTTTCAACAGCCTGAACTATGATGTTGCA	224
Qy	181	GCCAAGAAGAGAAAGAAGGACATGCTGAATAGCAAAACCAAACTCAGTATTTCCACCAA	240
Db	225	GCCAAGAAGAGAAAGAAGGACATGCTGAATAGCAAAACCAAACTCAGTATTTCCACCAA	284
Qy	241	GAAAAATGGATCTATGTTTCAAAAGGAAGTACTAAAGAGCGCCATGGATATTGCACCCTG	300
Db	285	GAAAAATGGATCTATGTTTCAAAAGGAAGTACTAAAGAGCGCCATGGATATTGCACCCTG	344
Qy	301	GGGGAAGCTTTCAACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTTAAC	360
Db	345	GGGGAAGCTTTCAACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTTAAC	404
Qy	361	TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATC	420
Db	405	TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATC	464
Qy	421	GCCCCAAAAGAACTTCATGAATATTTTGGAAAAGTGGTACTGAAAGTCCTTGAAGACCAG	480
Db	465	GCCCCAAAAGAACTTCATGAATATTTTGGAAAAGTGGTACTGAAAGTCCTTGAAGACCAG	524
Qy	481	CAAAACATTAGACTAATAAGGGAAGTACTCCAGACCCTCTACACATCCTTATGTACACTG	540
Db	525	CAAAACATTAGACTAATAAGGGAAGTACTCCAGACCCTCTACACATCCTTATGTACACTG	584
Qy	541	GTCCAAAGAGTCGGCAAGTCTGTGCTGGTCGGGAACATTAACATGTGGGTGTATCGGATG	600
Db	585	GTCCAAAGAGTCGGCAAGTCTGTGCTGGTCGGGAACATTAACATGTGGGTGTATCGGATG	644
Qy	601	GAGACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTCAGATCACCAGG	651
Db	645	GAGACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTCAGATCACCAGG	695

```
; Sequence 1011, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and Polypeptides
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SEQ ID NO 1011
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)..(809)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(828)
; OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-1011
```

Alignment Scores:

Pred. No.:	3.06e-130	Length:	828
Score:	1136.00	Matches:	217
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	60.07%	Indels:	0
DB:	4	Gaps:	0

US-10-061-043A-35 (1-355) x US-09-620-312D-1011 (1-828)

Qy	1	MetProPheLeuGlyGlnAspTrpArgSerProGlyGlnAsnTrpValLysThrAlaAsp	20
Db	45	ATGCCATTCCCTCGGGCAGGACTGGCGGTCCCCGGGGCAGAACTGGGTGAAGACGGCCGAC	104
Qy	21	GlyTrpLysArgPheLeuAspGluLysSerGlySerPheValSerAspLeuSerSerTyr	40
Db	105	GGCTGGAAGCGCTTCCTGGATGAGAAGAGCGGCAGTTTCGTGAGCGACCTCAGCAGTTAC	164
Qy	41	CysAsnLysGluValTyrAsnLysGluAsnLeuPheAsnSerLeuAsnTyrAspValAla	60
Db	165	TGCAACAAGGAGGTATACAATAAGGAGAATCTTTTCAACAGCCTGAACTATGATGTTGCA	224
Qy	61	AlaLysLysArgLysLysAspMetLeuAsnSerLysThrLysThrGlnTyrPheHisGln	80
Db	225	GCCAGAAGAGAAAGAAGGACATGCTGAATAGCAAAACCAAACTCAGTATTTCCACCAA	284
Qy	81	GluLysTrpIleTyrValHisLysGlySerThrLysGluArgHisGlyTyrCysThrLeu	100
Db	285	GAAAAATGGATCTATGTTCAAAAGGAAGTACTAAAGAGCGCCATGGATATTGCACCCTG	344
Qy	101	GlyGluAlaPheAsnArgLeuAspPheSerThrAlaIleLeuAspSerArgArgPheAsn	120
Db	345	GGGGAAGCTTTCACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTTAAC	404

Qy 121 TyrValValArgLeuLeuGluLeuIleAlaLysSerGlnLeuThrSerLeuSerGlyIle 140
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 405 TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATC 464

 Qy 141 AlaGlnLysAsnPheMetAsnIleLeuGluLysValValLeuLysValLeuGluAspGln 160
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 465 GCCCAAAGAACTTCATGAATATTTTGGAAAAAGTGGTACTGAAAGTCCTTGAAGACCAG 524

 Qy 161 GlnAsnIleArgLeuIleArgGluLeuLeuGlnThrLeuTyrThrSerLeuCysThrLeu 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 525 CAAACATTAGACTAATAAGGGAAGTACTCCAGACCCTCTACACATCCTTATGTACTG 584

 Qy 181 ValGlnArgValGlyLysSerValLeuValGlyAsnIleAsnMetTrpValTyrArgMet 200
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 585 GTCCAAAGAGTCGGCAAGTCTGTGCTGGTCGGGAACATTAACATGTGGGTGTATCGGATG 644

 Qy 201 GluThrIleLeuHisTrpGlnGlnGlnLeuAsnAsnIleGlnIleThrArg 217
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 645 GAGACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTCAGATCACCAGG 695

Db 365 GTCCAAAGAGTCGGCAAGTCTGTGCTGGTCGGGAACATTAACATGTGGGTGTATCGGATG 424

Qy 601 GAGACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTTCAGATCACCAGGCCTGCCTTC 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 425 GAGACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTTCAGATCACCAGGCCTGCCTTC 484

Qy 661 AAAGGCCTCACCTTCACTGACCTGCCTTTGTGCCTACAACCTGAACATCATGCAGAGGCTG 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 485 AAAGGCCTCACCTTCACTGACCTGCCTTTGTGCCTACAACCTGAACATCATGCAGAGGCTG 544

Qy 721 AGCGACGGGCGGGACCTGGTCAGCCTGGGCCAGGCTGCCCCGACCTGCACGTGCTCAGC 780
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 545 AGCGACGGGCGGGACCTGGTCAGCCTGGGCCA-GCTGCCCCGACCTGCACGTGCTCAGC 603

Qy 781 GAAGACCGGCTGCTGTGGAAGAAACTCTGCCAGTACCACTTCTCCGAGCGGCAGATCCGC 840
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 604 GAAGACCGGCTGCTGTGGAAGAAACTCTGCCAGTACCACTTCTCCGAGCGGCAGATCCGC 663

Qy 841 AAACGATTAATTCTGTCAGACAAAGGGCAGCTGGATTGGAAGAAGATGTATTTCAAACCTT 900
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 664 AAACGATTAATTCTGTCAGACAAAGGGCAGCTGGATTGGAAGAAGATGTATTTCAAACCTT 723

Qy 901 GTCCGATGTTACCCAAGGAAAGAGCAGTATGGAGATACCCTTCAGCTCTGCAAACACTGT 960
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 724 GTCCGATGTTACCCAAGGAAAGAGCAGTATGGAGATACCCTTCAGCTCTGCAAACACTGT 783

Qy 961 CACATCCTTTTCCTGGAAGGGCACTGACCATCCGTGCACTGCCAATAACCCAGAGAGCTGC 1020
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 784 CACATCCTTTTCCTGGAAGGGCACTGACCATCCGTGCACTGCCAATAACCCAGAGAGCTGC 843

Qy 1021 TCCGTTTCACTTTCACCCCAGGACTTTATCAACTTGTTCAGTTC 1065
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 844 TCCGTTTCACTTTCACCCCAGGACTTTATCAACTTGTTCAGTTC 888

ID AAF15631 standard; cDNA; 1302 BP.
 XX
 AC AAF15631;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:66.
 XX
 OS Homo sapiens.
 XX
 PN WO200055174-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US005988.
 XX
 PR 12-MAR-1999; 99US-0124270P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 XX
 PI Rosen CA, Ruben SM;
 XX
 SQ Sequence 1302 BP; 400 A; 297 C; 295 G; 307 T; 0 U; 3 Other;

Alignment Scores:

Pred. No.:	1.31e-150	Length:	1302
Score:	1515.00	Matches:	291
Percent Similarity:	98.98%	Conservative:	0
Best Local Similarity:	98.98%	Mismatches:	3
Query Match:	80.12%	Indels:	1
DB:	3	Gaps:	0

US-10-061-043A-35 (1-355) x AAF15631 (1-1302)

Qy	62	LysLysArgLysLysAspMetLeuAsnSerLysThrLysThrGlnTyrPheHisGlnGlu	81
Db	8	AAGAAGAGAAAGAAGGACATGCTGAATAGCAAAACCAAACTCAGTATTTCCACCAGGAA	67
Qy	82	LysTrpIleTyrValHisLysGlySerThrLysGluArgHisGlyTyrCysThrLeuGly	101
Db	68	AAATGGATCTATGTTCAAAAGGAAGTACTAMAGAGCGCCATGGATATTGCACCCTGGGG	127
Qy	102	GluAlaPheAsnArgLeuAspPheSerThrAlaIleLeuAspSerArgArgPheAsnTyr	121
Db	128	RAAGCTTTCAACAGACTGGACTTCTCAACTGCMATTCTGGATTCCAGAAGATTTAACTAC	187
Qy	122	ValValArgLeuLeuGluLeuIleAlaLysSerGlnLeuThrSerLeuSerGlyIleAla	141
Db	188	GTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATCGCC	247
Qy	142	GlnLysAsnPheMetAsnIleLeuGluLysValValLeuLysValLeuGluAspGlnGln	161
Db	248	CAAAAGAACTTCATGAATATTTTGAAAAAGTGGTACTGAAAGTCCTTGAAGACCAGCAA	307

Qy	162	AsnIleArgLeuIleArgGluLeuLeuGlnThrLeuTyrThrSerLeuCysThrLeuVal	181
Db	308	AACATTAGACTAATAAGGGAAGTACTCCAGACCTCTACACATCCTTATGTACACTGGTC	367
Qy	182	GlnArgValGlyLysSerValLeuValGlyAsnIleAsnMetTrpValTyrArgMetGlu	201
Db	368	CAAAGAGTCGGCAAGTCTGTGCTGGTCGGGAACATTAACATGTGGGTGTATCGGATGGAG	427
Qy	202	ThrIleLeuHisTrpGlnGlnGlnLeuAsnAsnIleGlnIleThrArgProAlaPheLys	221
Db	428	ACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTAGATCACCAGGCCTGCCTTCAA	487
Qy	222	GlyLeuThrPheThrAspLeuProLeuCysLeuGlnLeuAsnIleMetGlnArgLeuSer	241
Db	488	GGCCTCACCTTCACTGACCTGCCTTTGTGCCTACAACATCATGCAGAGGCTGAGC	547
Qy	242	AspGlyArgAspLeuValSerLeuGlyGlnAlaAlaProAspLeuHisValLeuSerGlu	261
Db	548	GACGGGCGGGACCTGGTCAGCCTGGGCCAGCT-GCCCCGACCTGCACGTGCTCAGCGAA	606
Qy	262	AspArgLeuLeuTrpLysLysLeuCysGlnTyrHisPheSerGluArgGlnIleArgLys	281
Db	607	GACCGGCTGCTGTGGAAGAACTCTGCCAGTACCCTTCTCCGAGCGGCAGATCCGCAA	666
Qy	282	ArgLeuIleLeuSerAspLysGlyGlnLeuAspTrpLysLysMetTyrPheLysLeuVal	301
Db	667	CGATTAATTCTGTCAGACAAAGGGCAGCTGGATTGGAAGAAGATGTATTTCAAACCTGTC	726
Qy	302	ArgCysTyrProArgLysGluGlnTyrGlyAspThrLeuGlnLeuCysLysHisCysHis	321
Db	727	CGATGTTACCCAAGGAAAGAGCAGTATGGAGATACCCTTCAGCTCTGCAAACACTGTCAC	786
Qy	322	IleLeuSerTrpLysGlyThrAspHisProCysThrAlaAsnAsnProGluSerCysSer	341
Db	787	ATCCTTTCTGGAAGGGCACTGACCATCCGTGCACTGCCAATAACCCAGAGAGCTGCTCC	846
Qy	342	ValSerLeuSerProGlnAspPheIleAsnLeuPheLysPhe	355
Db	847	GTTTCACTTTACCCCAGGACTTTATCAACTTGTTCAGTTC	888

ALIGNMENT

ID ADE24728 standard; cDNA; 2067 BP.
 XX
 AC ADE24728;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Mouse cDNA encoding F-box protein, Atrophin-1.
 XX
 OS Mus sp.
 XX
 PN US2003077288-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 16-JAN-2002; 2002US-00050686.
 XX
 PR 16-JAN-2001; 2001US-0262090P.
 XX
 PI Goldberg AL, Gomes MD, Lecker SH, Jagoe RT;
 XX
 SQ Sequence 2067 BP; 572 A; 512 C; 527 G; 456 T; 0 U; 0 Other;

Query Match 90.2%; Score 961; DB 9; Length 2067;
 Best Local Similarity 93.9%; Pred. No. 1.6e-271;
 Matches 1000; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy	1	ATGCCATTCTCGGGCAGGACTGGCGGTCCCCGGGCAGAACTGGGTGAAGACGGCCGAC	60
Db	328	ATGCCGTTCTTGGGCAGGACTGGCGGTCCCCGGGCAGAGCTGGGTGAAGACGGCGGAC	387
Qy	61	GGCTGGAAGCGCTTCCTGGATGAGAAGAGCGGCAGTTTCGTGAGCGACCTCAGCAGTTAC	120
Db	388	GGCTGGAAGCGCTTCTTGGATGAGAAAAGCGGCAGCTTCGTGAGCGACCTCAGCAGTTAC	447
Qy	121	TGCAACAAGGAGGTATACAATAAGGAGAATCTTTTCAACAGCCTGAACATATGATGTTGCA	180
Db	448	TGCAACAAGGAGGTATACAGTAAGGAGAATCTGTTTACAGCAGCCTGGACTACGACGTCGCA	507
Qy	181	GCCAAGAAGAGAAAGAAGGACATGCTGAATAGCAAAACCAAACTCAGTATTTCCACCAA	240
Db	508	GCCAAGAAGAGAAAGAAAGACATTGAGAACAGCAAAACCAAACTCAGTACTTCCATCAA	567
Qy	241	GAAAAATGGATCTATGTTTACAAAGGAAGTACTAAAGAGCGCCATGGATATTGCACCCTG	300
Db	568	GAAAAGTGGATCTATGTTTACAAAGGAAGTACGAAGGAGCGCCATGGATACTGTACTTTG	627
Qy	301	GGGGAAGCTTTCAACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTTAAC	360
Db	628	GGGGAAGCTTTCAACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTTAAC	687
Qy	361	TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATC	420
Db	688	TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATC	747
Qy	421	GCCCCAAAGAACTTCATGAATATTTTGGAAAAAGTGGTACTGAAAGTCCTTGAAGACCAG	480
Db	748	GCCCCAAAGAACTTCATGAATATTTTGGAAAAAGTGGTACTGAAAGTCCTTGAAGACCAG	807

Qy 481 CAAAACATTAGACTAATAAGGGAACTACTCCAGACCCTCTACACATCCTTATGTACTG 540
 |||
 Db 808 CAAAACATTAGACTAATAAGGGAACTACTCCAGACCCTCTACACATCCTTATGTACTG 867
 |||
 Qy 541 GTCCAAAGAGTCGGCAAGTCTGTGCTGGTCGGGAACATTAACATGTGGGTGTATCGGATG 600
 |||
 Db 868 GTCCAAAGAGTCGGCAAGTCTGTGCTGGTCGGGAACATTAACATGTGGGTGTATCGGATG 927
 |||
 Qy 601 GAGACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTCAGATCACCAGGCCTGCCTTC 660
 |||
 Db 928 GAGACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTCAGATCACCAGGCCTGCCTTC 987
 |||
 Qy 661 AAAGGCCTCACCTTCACTGACCTGCCTTTGTGCCTACAACATGAACATCATGCAGAGGCTG 720
 |||
 Db 988 AAAGGCCTCACCTTCACTGACCTGCCTTTGTGCCTACAACATGAACATCATGCAGAGGCTG 1047
 |||
 Qy 721 AGCGACGGGCGGGACCTGGTCAGCCTGGGCCAGGCTGCCCCGACCTGCACGTGCTCAGC 780
 |||
 Db 1048 AGCGACGGGCGGGACCTGGTCAGCCTGGGCCAGGCGCCCGACCTGCATGTGCTCAGT 1107
 |||
 Qy 781 GAAGACCGGCTGCTGTGGAAGAACTCTGCCAGTACCATTCTCCGAGCGGCAGATCCGC 840
 || |||
 Db 1108 GAGGACCGGCTACTGTGGAAGAGACTCTGCCAGTACCATTCTCAGAGAGGCAGATTTCGC 1167
 || |||
 Qy 841 AAACGATTAATTCTGTCTCAGACAAAGGGCAGCTGGATTGGAAGAAGATGTATTTCAAACCTT 900
 || || || || || |||
 Db 1168 AAGCGTTTGATCTTGTCTGACAAAGGGCAGCTGGATTGGAAGAAGATGTATTTTAAGCTT 1227
 || || || || || |||
 Qy 901 GTCCGATGTTACCCAAGGAAAGAGCAGTATGGAGATACCCTTCAGCTCTGCAAACACTGT 960
 || |||
 Db 1228 GTACGATGTTACCCAAGAAGAGAGCAGTATGGGGTCACCCTGCAGCTTTGCAAACACTGC 1287
 || |||
 Qy 961 CACATCCTTTCTGGAAGGGCACTGACCATCCGTGCACTGCCAATAACCCAGAGAGCTGC 1020
 |||| || |||
 Db 1288 CACATTCTCTCCTGGAAGGGCACTGACCATCCGTGACGGCCAACAACCCAGAGAGCTGC 1347
 |||| || |||
 Qy 1021 TCCGTTTCACTTTACCCCAGGACTTTATCAACTTGTTCAAGTTC 1065
 |||| |||
 Db 1348 TCCGTCTCACTTTCCCTCAAGACTTTATCAATTTGTTCAAGTTC 1392
 |||| |||

ID ADE24728 standard; cDNA; 2067 BP.
 XX
 AC ADE24728;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Mouse cDNA encoding F-box protein, Atrophin-1.
 XX
 OS Mus sp.
 XX
 PN US2003077288-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 16-JAN-2002; 2002US-00050686.
 XX
 PR 16-JAN-2001; 2001US-0262090P.
 XX
 PI Goldberg AL, Gomes MD, Lecker SH, Jagoe RT;
 XX
 SQ Sequence 2067 BP; 572 A; 512 C; 527 G; 456 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.92e-185	Length:	2067
Score:	1846.00	Matches:	346
Percent Similarity:	99.44%	Conservative:	7
Best Local Similarity:	97.46%	Mismatches:	2
Query Match:	97.62%	Indels:	0
DB:	9	Gaps:	0

US-10-061-043A-35 (1-355) x ADE24728 (1-2067)

Qy	1	MetProPheLeuGlyGlnAspTrpArgSerProGlyGlnAsnTrpValLysThrAlaAsp	20
Db	328	ATGCCGTTCTTGGGCAGGACTGGCGGTCCCCGGGCCAGAGCTGGGTGAAGACGGCGGAC	387
Qy	21	GlyTrpLysArgPheLeuAspGluLysSerGlySerPheValSerAspLeuSerSerTyr	40
Db	388	GGCTGGAAGCGCTTCTTGGATGAGAAAAGCGGCAGCTTCGTGAGCGACCTCAGCAGTTAC	447
Qy	41	CysAsnLysGluValTyrAsnLysGluAsnLeuPheAsnSerLeuAsnTyrAspValAla	60
Db	448	TGCAACAAGGAGGTATACAGTAAGGAGAATCTGTTTCAGCAGCCTGGACTACGACGTCCGA	507
Qy	61	AlaLysLysArgLysLysAspMetLeuAsnSerLysThrLysThrGlnTyrPheHisGln	80
Db	508	GCCAAGAAGAGAAAGAAAGACATTTCAGAACAGCAAAACCAAACTCAGTACTTCCATCAA	567
Qy	81	GluLysTrpIleTyrValHisLysGlySerThrLysGluArgHisGlyTyrCysThrLeu	100
Db	568	GAAAAGTGGATCTATGTTTACAAAGGAAGTACGAAGGAGCGCCATGGATACTGTACTTTG	627
Qy	101	GlyGluAlaPheAsnArgLeuAspPheSerThrAlaIleLeuAspSerArgArgPheAsn	120
Db	628	GGGGAAGCTTTCAACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTTAAC	687

Qy 121 TyrValValArgLeuLeuGluLeuIleAlaLysSerGlnLeuThrSerLeuSerGlyIle 140
 |||
 Db 688 TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATC 747

Qy 141 AlaGlnLysAsnPheMetAsnIleLeuGluLysValValLeuLysValLeuGluAspGln 160
 |||
 Db 748 GCCCAAAGAAGCTTCATGAATATTTTGGAAAAAGTGGTACTGAAAGTCCTTGAAGACCAG 807

Qy 161 GlnAsnIleArgLeuIleArgGluLeuLeuGlnThrLeuTyrThrSerLeuCysThrLeu 180
 |||
 Db 808 CAAACATTAGACTAATAAGGGAAGTACTCCAGACCCTCTACACATCCTTATGTACACTG 867

Qy 181 ValGlnArgValGlyLysSerValLeuValGlyAsnIleAsnMetTrpValTyrArgMet 200
 |||
 Db 868 GTCCAAAGAGTCGGCAAGTCTGTGCTGGTGGGAACATTAACATGTGGGTGTATCGGATG 927

Qy 201 GluThrIleLeuHisTrpGlnGlnGlnLeuAsnAsnIleGlnIleThrArgProAlaPhe 220
 |||
 Db 928 GAGACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTGATCACCAGGCCTGCCTTC 987

Qy 221 LysGlyLeuThrPheThrAspLeuProLeuCysLeuGlnLeuAsnIleMetGlnArgLeu 240
 |||
 Db 988 AAAGGCCTCACCTTCACTGACCTGCCTTTGTGCCTACAACATGATGCAGAGGCTG 1047

Qy 241 SerAspGlyArgAspLeuValSerLeuGlyGlnAlaAlaProAspLeuHisValLeuSer 260
 |||
 Db 1048 AGCGACGGGCGGGACCTGGTCAGCCTGGGCCAGGCAGCCCCAGACCTGCATGTGCTCAGT 1107

Qy 261 GluAspArgLeuLeuTrpLysLysLeuCysGlnTyrHisPheSerGluArgGlnIleArg 280
 |||::|
 Db 1108 GAGGACCGGCTACTGTGGAAGAGACTCTGCCAGTACCACTTCTCAGAGAGGCAGATTTCGC 1167

Qy 281 LysArgLeuIleLeuSerAspLysGlyGlnLeuAspTrpLysLysMetTyrPheLysLeu 300
 |||
 Db 1168 AAGCGTTTGATCTTGTCTGACAAAGGGCAGCTGGATTGGAAGAAGATGTATTTTAAGCTT 1227

Qy 301 ValArgCysTyrProArgLysGluGlnTyrGlyAspThrLeuGlnLeuCysLysHisCys 320
 |||::|
 Db 1228 GTACGATGTTACCCAAGAAGAGAGCAGTATGGGGTCACCCTGCAGCTTTGCAAACACTGC 1287

Qy 321 HisIleLeuSerTrpLysGlyThrAspHisProCysThrAlaAsnAsnProGluSerCys 340
 |||
 Db 1288 CACATTCTCTCCTGGAAGGGCACTGACCATCCGTGCACGGCCAACAACCCAGAGAGCTGC 1347

Qy 341 SerValSerLeuSerProGlnAspPheIleAsnLeuPheLysPhe 355
 |||
 Db 1348 TCCGTCTCACTTCCCCTCAAGACTTTATCAATTTGTTCAAGTTC 1392